



1/19

FIGURE 1A

-28	AGTATTGTTGTCGTGTTTGCCCTTGTAAGGCGGTCATCCCTCAAGTGATCACTTAGTCAA	31
-80		-40
-20		-1
32	GAGTCCTGGAATCTTTTCACATCCACTATGAACACCTCTCACCTCCTGGCCTTGCTGCTC	91
-8		20
	M N T S H L L A L L L	11
40		80
60		
80		
100		120
120		140
140		
160		180
180		200
200		
220		
240		
260		
280		
300		
320		
340		
360		
380		
400		
420		
440		
460		
480		
500		
520		
540		
560		
580		
600		
620		
640		
660		
680		
700		
720		
740		
760		
780		
800		
820		
840		
860		
880		
900		
920		
940		
960		
980		
1000		



2/19

FIGURE 1B

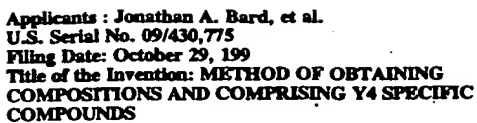
272	AAAGCCAAACGTGACCAACCTGCTTATCGCCAAACCTGGCCCTTCTCTGACTTCCTCATGTGC	220	240	260	331
72	K A N V T N L L I A N L A F S D F L M C				91
280		300	320		
332	CTCCTCTGCCAGCCGCTGACCGCCGCTACACCATCATGGACTACTGGATCTTTGGAGAG				391
92	L L C Q P L T A V Y T I M D Y W I F G E				111
340		360	380		
392	ACCCTCTGCAAGATGTCGGCCCTTCATCCAGTCCAGTGCGTGACGGTCTCCATCCTCTCG				451
112	T L C K M S A F I Q C M S V T V S I L S				131
400		420	440		
452	CTCGTCCTCGTGGCCCTGGAGAGGCATCAGCTCATCAACCCAAACAGGCTGGAAGCCC				511
132	L V L V A L E R H Q L I I N P T G W K P				151
460		480	500		
512	AGCATCTCACAGGCCCTACCTGGGGATTGTGCTCATCTGGGTCATTGCCCTGTGCTCCTCC				571
152	S I S Q A Y L G I V L I W V I A C V L S				171



3/19

FIGURE 1C

	520	540	560	
572	CTGCCCTTCCTGGCCAAACAGCATCCTGGAGAAATGTCTTCCACAAGAACCACTCCAAGGCT			631
172	L P F L A N S I L E N V F H K N H S K A			191
	580	600	620	
632	CTGGAGTTCCCTGGCAGATAAGGTGGTCTGTACCGAGTCCTGGCCACTGGGCTCACCACCGC			691
192	L E F L A D K V V C T E S W P L A H H R			211
	640	660	680	
692	ACCATCTACACCACTTCCTGGCTCCTCTTCCAGTACTGCCCTCCCACTGGGCTTCATCCTG			751
212	T I Y T T F L L L L F Q Y C L P L G F I L			231
	700	720	740	
752	GTCTGTTATGCACGCATCTACCGGGCCCTGCAGAGGCGCGGCTGTTTCAACAAGGCG			811
232	V C Y A R I Y R R L Q R Q R Q G R V F H K G			251
	760	780	800	
812	ACCTACAGCTTGGGAGCTGGGCACATGAAGCAGGTCAATGTGTGCTGGTGGTGGTG			871
252	T Y S L R A G H M K Q V N V V L V V M V			271

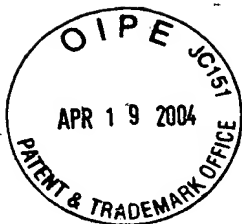


**4/19**

**FIGURE 1D**

872	GTGGCCTTTGCGGTGCTCTGGCTGCCTCTGTCATGTGTCAACAGCCTGGAAGACTGGCAC	820	840	860	931
272	V A F A V L W L P L H V F N S L E D W H				291
		880	900	920	
932	CATGAGGCCATCCCCCATCTGCCACGGGAACCTCATCTTCTTAGTGTGCCACTTGTCTTGCC				991
292	H E A I P I C H G N L I F L V C H L L A				311
		940	960	980	
992	ATGGCCTCCACCTGCGTCAACCCATTCATCTATGGCTTTCTCAACACCAACTTCAAGAAG				1051
312	M A S T C V N P F I Y G F L N T N F K K				331
		1000	1020	1040	
1052	GAGATCAAGGCCCTGGTGCTGACTTGCCAGCAGAGCGCCCCCTGGAGGAGTCGGAGCAT				1111
332	E I K A L V L T C Q Q S A P L E E S E H				351
		1060	1080	1100	
1112	CTGCCCTGTCCACAGTACATACGGAAGTCTCCAAAGGGTCCCTGAGGCTAAGTGGCAGG				1171
352	L P L S T V H T E V S K G S L R L S G R				371





6/19

FIGURE 2A

hp25a human Y1 rat Y1 mouse Y1	1	50				100				150				200			
		I				II				III				IV			
		MNTSHLLALL LPKSPQGENR SKPLGTPYNF SEHCQDSVDV MVFI VTSYSI				ETVVGVLGNL CLMCVTVRQK EKANVTNLLI ANLAFSDFIM CLLCQPLTAV				YTIMDYWIFG ETLCKMSAFI QCMSVTVSIL SLVLVALERH QLIINPTGKW				PSISQAYLGI VLIWVIACVL SLPFLANSIL			
		MN. STLF SQV ENHSVHSNFS EKNAQLLAFE NDDCHLPLAM IFTLALAYGA				VIILGVSGNL ALIIIIILKQK EMRNVTNILI VNLSFSDLLV AIMCLPFTFV				YTLMDHWVFG EAMCKLNPFV QCVSITVSIF SLVLI AVERH QLIINPRGWR				PNNRHAYVGI AVIWVLAVAS SLPFLIYQVM			
hp25a human Y1 rat Y1 mouse Y1	51	MN. STLF SRV ENYSVHYNVS E.NSPFLAFE NDDCHLPLAV IFTLALAYGA				VIILGVSGNL ALIIIIILKQK EMRNVTNILI VNLSFSDLLV AVMCLPFTFV				YTLMDHWVFG ETMCKLNPFV QCVSITVSIF SLVLI AVERH QLIINPRGWR				PNNRHAYIGI TVIWVLAVAS SLPFLVIYQIL			
		MN. STLF SKV ENHSIHYNAS E.NSPLLAFE NDDCHLPLAV IFTLALAYGA				VIILGVSGNL ALIIIIILKQK EMRNVTNILI VNLSFSDLLV AVMCLPFTFV				YTLMDHWVFG ETMCKLNPFV QCVSITVSIF SLVLI AVERH QLIINPRGWR				PNNRHAYIGI TVIWVLAVAS SLPFLVIYQIL			
hp25a human Y1 rat Y1 mouse Y1	101																
hp25a human Y1 rat Y1 mouse Y1	151																



7/19

FIGURE 2B

hp25a human Y1 rat Y1 mouse Y1	201	CTESWPLAHH RTIYTTFILL FQYCLPLGFI CFDQFPSSDSH RLSYTTLLLV LQYFGPLCFI CFDKFPSSDSH RLSYTTLLLV LQYFGPLCFI CFDKFPSSDSH RLSYTTLLLV LQYFGPLCFI	V	LVCYARIYRR LQRCGRVPHK FICYFKIYIR LKRRNNMMDK FICYFKIYIR LKRRNNMMDK FICYFKIYIR LKRRNNMMDK	250
hp25a human Y1 rat Y1 mouse Y1	251	GTYS.LRAGH MKQNVVIVV MVVAFVAVLWL MRDNKYRSSE TKRINIMLLS IVVAFVAVCWL IRDSKYRSSE TKRINVMLLS IVVAFVAVCWL IRDSKYRSSE TKRINIMLLS IVVAFVAVCWL	VI	PLHVFNSLED WHHEAIPICH PLTIFNTVFD WNHQIIATCN PLTIFNTVFD WNHQIIATCN PLTIFNTVFD WNHQIIATCN	300
hp25a human Y1 rat Y1 mouse Y1	301	GNIIFLVCHL LAMASTCVNP FIYGFNLNTNF HNLLFLLCHL TAMISTCVNP IFYGFNLKNF HNLLFLLCHL TAMISTCVNP IFYGFNLKNF HNLLFLLCHL TAMISTCVNP IFYGFNLKNF	VII	KKEIKALVLT CQQSAPLEES QRDLQFFNF CDFRSRDDDY QRDLQFFNF CDFRSRDDDY QRDLQFFNF CDFRSRDDDY	350



8/19

FIGURE 2C

hp25a	351	EHLPLSTVHT	EVSKGSLRLS	GRSNPI*....	.....	388
human Y1		ETIAMSTMHT	DVSKTSLKQA	SPVAFKKINN	NDDNEKI*	
rat Y1		ETIAMSTMHT	DVSKTSLKQA	SPVAFKKISM	N.DNEKI*	
mouse Y1		ETIAMSTMHT	DVSKTSLKQA	SPVAFKKISM	N.DNEKV*	





9/19

**FIGURE 3A**

-170                                      -150                                      -130

ATAGCTCTCAAGCCATAAGATATAAGTAGCTAAGAATTGTCTCCCTCTCCCTGTCCCTTG

-110                                      -90                                      -70

TTCTTACCTGGTTCCATTTTACATGCCTGGACCTTTGAGTTCCATTTGTTTGTGTTTGCAG

-50                                      -30                                      -10

GCTACACTCAGAAGTGGGCCCTTTAGTCTTGAAGTTCCTGGTCTTCTCACACCCACCATG

M

10                                      30                                      50

AATACCTCTCATCTCATGGCCTCCCTTTCTCCGGCATTTCCTACAAGGTAAGAATGGGACC

N T S H L M A S L S P A F L Q G K N G T

70                                      90                                      110

AACCCACTGGATTCCCTCTATAATCTCTCTGACGGCTGCCAGGATTCCGGCAGATCTGTTG

N P L D S L Y N L S D G C Q D S A D L L

130                                      150                                      170

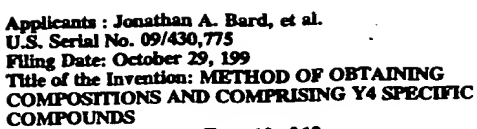
GCCTTCATCATCACCACCTACAGCGTTGAGACCGTCTTGGGGTCTTAGGAAACCTCTGC

A F I I T T Y S V E T V L G V L G N L C

190                                      210                                      230

TTGATATTTGTGACCACAAGGCAAAAGGAAAAGTCCAATGTGACCAACCTACTCATTGCC

L I F V T T R Q K E K S N V T N L L I A



10/19

250 270 290

AACCTGGCCTTCTCTGACTTCCTCATGTGTCTCATCTGCCAGCCGCTCACGGTCACCTAC  
N L A F S D F L M C L I C Q P L T V T Y

310 330 350

ACCATCATGGACTACTGGATCTTCGGCGAAGTCCTTTGCAAGATGTTAACGTTTCATCCAG  
T I M D Y W I F G E V L C K M L T F I Q

370 390 410

TGTATGTCGGTGACAGTCTCCATCCTCTCACTGGTCCTTGTGGCCCTGGAGAGGCACCAG  
C M S V T V S I L S L V L V A L E R H Q

430 450 470

CTCATTATCAACCCGACTGGCTGGAAACCCAGCATTTCCTCCAGGCCTACCTGGGGATTGTG  
L I I N P T G W K P S I S Q A Y L G I V

490 510 530

GTCATCTGGTTCATTTCTTGTTCCTCTCCTTGCCCTTCCTGGCCAATAGCATCCTGAAC  
V I W F I S C F L S L P F L A N S I L N

550 570 590

GACCTCTTCCACTACAACCACTCTAAGGTTGTGGAGTTTCTGGAAGACAAGGTTGTCTGC  
D L F H Y N H S K V V E F L E D K V V C

610 630 650

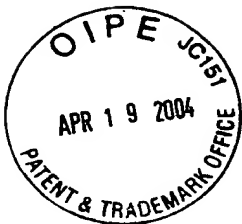
TTTGTGTCCTGGTCCTCGGATCACCACCGCCTCATCTACACCACCTTTCTGCTGCTCTTC  
F V S W S S D H H R L I Y T T F L L L F



11/19

**FIGURE 3C**

670	690	710
CAATACTGCGTCCCTCTGGCCTTCATCCTGGTCTGCTACATGCGTATCTATCAGCGCCTG		
Q Y C V P L A F I L V C Y M R I Y Q R L		
730	750	770
CAGAGGCAGAGGCGTGCGTTCCACACGCACACTTGCAGCTCACGAGTGGGGCAGATGAAG		
Q R Q R R A F H T H T C S S R V G Q M K		
790	810	830
CGGATCAATGGCATGCTCATGGCAATGGTGACTGCCTTTGCAGTTCTCTGGCTGCCCCCTG		
R I N G M L M A M V T A F A V L W L P L		
850	870	890
CATGTGTTCAACACTCTGGAGGACTGGTACCAGGAAGCCATCCCTGCTTGCCATGGCAAC		
H V F N T L E D W Y Q E A I P A C H G N		
910	930	950
CTCATCTTCTTGATGTGCCACCTGTTTGCCATGGCTTCCACCTGTGTCAACCCTTTCATC		
L I F L M C H L F A M A S T C V N P F I		
970	990	1010
TATGGCTTTCTCAACATCAACTTCAAGAAGGACATCAAGGCTCTGGTTCTGACCTGCCGT		
Y G F L N I N F K K D I K A L V L T C R		
1030	1050	1070
TGCAGGCCACCTCAAGGGGAGCCTGAGCCTCTGCCCCTGTCCACTGTGCACACGGACCTC		
C R P P Q G E P E P L P L S T V H T D L		



12/19

FIGURE 3D

1090	1110	1130
TCCAAGGATCTATGAGGATGGGTAGCAAGTCTAACGTCATGTAGTCATGTCTAGGCTCT		
S K G S M R M G S K S N V M *		
1150	1170	1190
TCCGCCATTCTTCGACACACCCCTTTCACCTGAGCTAAGTAGACACAAATGCAAGCTGTG		
1210	1230	1250
GTATCATCCTGCCATTCTGTGTCCTTTGGGGCCAGACAGCGCGCAAGAGACTTGAAGCTT		



13/19

FIGURE 4

1		50
Y4rat	MNTSHLMASL SPAFLQGKNG TNPLDSLYNL SDGCQDSADL LAFIITTYSV	
Y4hum	MNTSHLLALL LPKSPQGENR SKPLGTPYNF SEHCQDSVDV MVFIVTSYSI	
51		100
	I	II
Y4rat	ETVLGVLGNL CLIFVTTRQK EKSNTVNLLI ANLAFSDFLM CLICQPLTVT	
Y4hum	ETVVGVLGNL CLMCVTVRQK EKANVTNLLI ANLAFSDFLM CLLCQPLTAV	
101		150
	III	
Y4rat	YTIMDYWIFG EVLCKMLTFI QCMSVTVSIL SLVLVALERH QLIINPTGWK	
Y4hum	YTIMDYWIFG ETLCKMSAFI QCMSVTVSIL SLVLVALERH QLIINPTGWK	
151		200
	IV	
Y4rat	PSISQAYLGI VVIWFISCFL SLPFLANSIL NDLFHYNHSHK VVEFLEDKVV	
Y4hum	PSISQAYLGI VLIWVIACVL SLPFLANSIL ENVFHKNHSHK ALEPLADKVV	
201		250
	V	
Y4rat	CFVSWSSDHH RLIYTTFLLL FQYCVPLAFI LVCYMRIYQR LQRQRRAFHT	
Y4hum	CTESWPLAHH RTIYTTFLLL FQYCLPLGFI LVCYARIYRR LQRQGRVFHK	
251		300
	VI	
Y4rat	HTCSSRVGQM KRINGMLMAM VTAPAVLWLP LHVFNLTLEDW YQEAIPACHG	
Y4hum	GTYSLRAGHM KQVNVVLVVM VVAPAVLWLP LHVFNLSLEDW HHEAIPICHG	
301		350
	VII	
Y4rat	NLIFLMCHLF AMASTCVNPF IYGFLNINFK KDIKALVLTC RCRPPQGEPE	
Y4hum	NLIFLVCHLL AMASTCVNPF IYGFLNTNFK KEIKALVLTC QQSAPLEESE	